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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Mon Oct 01 18:08:24 EDT 2007

=====

Application No: 10566944 Version No: 1.0

Input Set:**Output Set:**

Started: 2007-09-14 12:26:12.517
Finished: 2007-09-14 12:26:29.678
Elapsed: 0 hr(s) 0 min(s) 17 sec(s) 161 ms
Total Warnings: 108
Total Errors: 281
No. of SeqIDs Defined: 192
Actual SeqID Count: 192

| Error code | Error Description |
|------------|---|
| E 355 | Empty lines found between the amino acid numbering and the |
| E 321 | No. of Bases conflict, this line has no nucleotides SEQID (1) |
| E 300 | Invalid codon found Ile SEQID (1) POS: 97 |
| E 300 | Invalid codon found Glu SEQID (1) POS: 100 |
| E 300 | Invalid codon found Asn SEQID (1) POS: 103 |
| E 300 | Invalid codon found Tyr SEQID (1) POS: 106 |
| E 300 | Invalid codon found Gln SEQID (1) POS: 109 |
| E 300 | Invalid codon found Gly SEQID (1) POS: 112 |
| E 300 | Invalid codon found Arg SEQID (1) POS: 115 |
| E 300 | Invalid codon found Asp SEQID (1) POS: 118 |
| E 300 | Invalid codon found Ala SEQID (1) POS: 121 |
| E 300 | Invalid codon found Thr SEQID (1) POS: 124 |
| E 300 | Invalid codon found Asp SEQID (1) POS: 127 |
| E 300 | Invalid codon found Ala SEQID (1) POS: 130 |
| E 300 | Invalid codon found Phe SEQID (1) POS: 133 |
| E 300 | Invalid codon found Met SEQID (1) POS: 136 |
| E 300 | Invalid codon found Val SEQID (1) POS: 139 |
| E 300 | Invalid codon found Met SEQID (1) POS: 142 |
| E 355 | Empty lines found between the amino acid numbering and the |
| E 321 | No. of Bases conflict, this line has no nucleotides SEQID (1) |

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| Error code | Error Description |
|------------|---|
| E 300 | Invalid codon found Leu SEQID (1) POS: 481 |
| E 300 | Invalid codon found Val SEQID (1) POS: 484 |
| E 300 | Invalid codon found Gly SEQID (1) POS: 487 |
| E 300 | Invalid codon found Leu SEQID (1) POS: 490 This error has occurred more than 20 times, will not be displayed |
| E 355 | Empty lines found between the amino acid numbering and the |
| E 321 | No. of Bases conflict, this line has no nucleotides SEQID (1) |
| E 355 | Empty lines found between the amino acid numbering and the |
| E 321 | No. of Bases conflict, this line has no nucleotides SEQID (1) |
| W 402 | Undefined organism found in <213> in SEQ ID (11) |
| W 402 | Undefined organism found in <213> in SEQ ID (12) |
| W 402 | Undefined organism found in <213> in SEQ ID (13) |
| W 402 | Undefined organism found in <213> in SEQ ID (14) |
| E 355 | Empty lines found between the amino acid numbering and the |
| E 321 | No. of Bases conflict, this line has no nucleotides SEQID (19) |
| E 355 | Empty lines found between the amino acid numbering and the |
| E 321 | No. of Bases conflict, this line has no nucleotides SEQID (19) |
| E 355 | Empty lines found between the amino acid numbering and the |
| E 321 | No. of Bases conflict, this line has no nucleotides SEQID (19) |
| E 355 | Empty lines found between the amino acid numbering and the |
| E 321 | No. of Bases conflict, this line has no nucleotides SEQID (19) |
| E 336 | Empty lines found between the proteins and the dna |
| E 336 | Empty lines found between the proteins and the dna |

Input Set :

Output Set :

Started: 2007-09-14 12:26:12.517

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Elapsed: 0 hr(s) 0 min(s) 17 sec(s) 161 ms

Total Warnings: 108

Total Errors: 281

No. of SeqIDs Defined: 192

Actual SeqID Count: 192

| Error code | Error Description |
|------------|--|
| E 336 | Empty lines found between the proteins and the dna |
| E 336 | Empty lines found between the proteins and the dna |
| E 336 | Empty lines found between the proteins and the dna |
| E 336 | Empty lines found between the proteins and the dna |
| E 336 | Empty lines found between the proteins and the dna |
| E 336 | Empty lines found between the proteins and the dna |
| E 336 | Empty lines found between the proteins and the dna |
| E 336 | Empty lines found between the proteins and the dna |
| E 336 | Empty lines found between the proteins and the dna |
| E 336 | Empty lines found between the proteins and the dna |
| E 336 | Empty lines found between the proteins and the dna |
| E 336 | Empty lines found between the proteins and the dna |
| E 336 | Empty lines found between the proteins and the dna |
| E 336 | Empty lines found between the proteins and the dna |
| E 336 | Empty lines found between the proteins and the dna |
| E 336 | Empty lines found between the proteins and the dna |
| E 336 | Empty lines found between the proteins and the dna |
| E 336 | Empty lines found between the proteins and the dna This error has occured more than 20 times, will not be displayed |
| E 355 | Empty lines found between the amino acid numbering and the |
| E 321 | No. of Bases conflict, this line has no nucleotides SEQID (26) |
| W 402 | Undefined organism found in <213> in SEQ ID (29) |
| W 402 | Undefined organism found in <213> in SEQ ID (30) |

Input Set:

Output Set:

Started: 2007-09-14 12:26:12.517

Finished: 2007-09-14 12:26:29.678

Elapsed: 0 hr(s) 0 min(s) 17 sec(s) 161 ms

Total Warnings: 108

Total Errors: 281

No. of SeqIDs Defined: 192

Actual SeqID Count: 192

| Error code | Error Description |
|------------|---|
| E 355 | Empty lines found between the amino acid numbering and the |
| E 321 | No. of Bases conflict, this line has no nucleotides SEQID (30) |
| W 402 | Undefined organism found in <213> in SEQ ID (33) |
| W 402 | Undefined organism found in <213> in SEQ ID (34) |
| W 402 | Undefined organism found in <213> in SEQ ID (35) |
| W 402 | Undefined organism found in <213> in SEQ ID (36) |
| W 402 | Undefined organism found in <213> in SEQ ID (41) |
| W 402 | Undefined organism found in <213> in SEQ ID (42) |
| E 355 | Empty lines found between the amino acid numbering and the |
| E 321 | No. of Bases conflict, this line has no nucleotides SEQID (42) |
| E 355 | Empty lines found between the amino acid numbering and the |
| E 321 | No. of Bases conflict, this line has no nucleotides SEQID (46) |
| E 355 | Empty lines found between the amino acid numbering and the |
| E 321 | No. of Bases conflict, this line has no nucleotides SEQID (58) |
| W 402 | Undefined organism found in <213> in SEQ ID (67) |
| W 402 | Undefined organism found in <213> in SEQ ID (68) |
| W 402 | Undefined organism found in <213> in SEQ ID (69) |
| W 402 | Undefined organism found in <213> in SEQ ID (70) |
| W 402 | Undefined organism found in <213> in SEQ ID (71) |
| W 402 | Undefined organism found in <213> in SEQ ID (72) |
| W 402 | Undefined organism found in <213> in SEQ ID (73) |
| W 402 | Undefined organism found in <213> in SEQ ID (74) |
| | This error has occurred more than 20 times, will not be displayed |

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Output Set:

Started: 2007-09-14 12:26:12.517

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Elapsed: 0 hr(s) 0 min(s) 17 sec(s) 161 ms

Total Warnings: 108

Total Errors: 281

No. of SeqIDs Defined: 192

Actual SeqID Count: 192

| Error code | Error Description |
|------------|---|
| W 213 | Artificial or Unknown found in <213> in SEQ ID (115) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (116) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (121) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (121) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (122) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (122) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (123) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (123) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (124) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (124) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (125) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (125) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (126) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (126) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (127) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (127) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (128) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (128) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (129) |

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| Error code | Error Description |
|------------|---|
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (129) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (130) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (130) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (139) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (140) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (141) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (142) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (143) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (143) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (144) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (144) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (145) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (145) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (146) This error has occurred more than 20 times, will not be displayed |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (146) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (147) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (148) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (149) |

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| Error code | Error Description |
|------------|--|
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (150) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (151) |
| E 224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (152) This error has occurred more than 20 times, will not be displayed |

SEQUENCE LISTING

<110> Zank, Thorsten
 Bauer, Jorg
 Cirpus, Petra
 Abbadi, Amine
 Heinz, Ernst
 Qiu, Xiao
 Vrinten, Patricia
 Sperling, Petra
 Domergue, Frederic
 Meyer, Astrid
 Kirsch, Jelena

<120> METHOD FOR THE PRODUCTION OF MULTIPLE-UNSATURATED FATTY ACIDS IN
 TRANSGENIC ORGANISMS

<130> 12810-00193-US

<140> 10566944
 <141> 2007-09-14

<150> DE 103 35 992.3
 <151> 2003-08-01

<150> DE 103 44 557.9
 <151> 2003-09-24

<150> DE 103 47 869.8
 <151> 2003-10-10

<150> DE 103 59 593.7
 <151> 2003-12-18

<150> DE 10 2004 009 457.8
 <151> 2004-02-27

<150> DE 10 2004 012 370.5
 <151> 2004-03-13

<150> DE 10 2004 024 014.0
 <151> 2004-05-14

<160> 192

<170> PatentIn version 3.1

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<223> delta8-desaturase

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|---|----|
| atg aag tca aag cgc caa gcg ctt ccc ctt aca att gat gga aca aca | 48 |
| Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr | |
| 1 5 10 15 | |

| | |
|---|----|
| tat gat gtg tct gcc tgg gtc aat ttc cac cct ggt ggt gcg gaa att | 96 |
| Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile | |
| 20 25 30 | |

| | |
|---|-----|
| ata gag aat tac caa gga agg gat gcc act gat gcc ttc atg gtt atg | 144 |
| Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met | |
| 35 40 45 | |

| | |
|---|-----|
| cac tct caa gaa gcc ttc gac aag ctc aag cgc atg ccc aaa atc aat | 192 |
| His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn | |
| 50 55 60 | |

| | |
|---|-----|
| ccc agt tct gag ttg cca ccc cag gct gca gtg aat gaa gct caa gag | 240 |
| Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu | |
| 65 70 75 80 | |

| | |
|---|-----|
| gat ttc cgg aag ctc cga gaa gag ttg atc gca act ggc atg ttt gat | 288 |
| Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp | |
| 85 90 95 | |

| | |
|---|-----|
| gcc tcc ccc ctc tgg tac tca tac aaa atc agc acc aca ctg ggc ctt | 336 |
| Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu | |
| 100 105 110 | |

| | |
|---|-----|
| gga gtg ctg ggt tat ttc ctg atg gtt cag tat cag atg tat ttc att | 384 |
| Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile | |
| 115 120 125 | |

| | |
|---|-----|
| ggg gca gtg ttg ctt ggg atg cac tat caa cag atg ggc tgg ctt tct | 432 |
| Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser | |
| 130 135 140 | |

| | |
|---|-----|
| cat gac att tgc cac cac cag act ttc aag aac cgg aac tgg aac aac | 480 |
| His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn | |
| 145 150 155 160 | |

| | |
|---|-----|
| ctc gtg gga ctg gta ttt ggc aat ggt ctg caa ggt ttt tcc gtg aca | 528 |
| Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr | |
| 165 170 175 | |

| | |
|---|-----|
| tgc tgg aag gac aga cac aat gca cat cat tcg gca acc aat gtt caa | 576 |
| Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln | |
| 180 185 190 | |

| | |
|---|-----|
| ggg cac gac cct gat att gac aac ctc ccc ctc tta gcc tgg tct gag | 624 |
| Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu | |
| 195 200 205 | |

| | |
|---|------|
| gat gac gtc aca cgg gcg tca ccg att tcc cgc aag ctc att cag ttc | 672 |
| Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe | |
| 210 215 220 | |
| | |
| cag cag tat tat ttc ttg gtc atc tgt atc ttg ttg cgg ttc att tgg | 720 |
| Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp | |
| 225 230 235 240 | |
| | |
| tgt ttc cag agc gtg ttg acc gtg cgc agt ctg aag gac aga gat aac | 768 |
| Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn | |
| 245 250 255 | |
| | |
| caa ttc tat cgc tct cag tat aag aag gag gcc att ggc ctc gcc ctg | 816 |
| Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu | |
| 260 265 270 | |
| | |
| cat tgg aca ttg aag gcc ctg ttc cac tta ttc ttt atg ccc agc atc | 864 |
| His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile | |
| 275 280 285 | |
| | |
| ctc aca tcg ctg ttg gta ttt ttc gtt tcg gag ctg gtt ggc ggc ttc | 912 |
| Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe | |
| | |
| 290 295 300 | |
| | |
| ggc att gcg atc gtg gtg ttc atg aac cac tac cca ctg gag aag atc | 960 |
| Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile | |
| 305 310 315 320 | |
| | |
| ggg gac tcg gtc tgg gat ggc cat gga ttc tcg gtt ggc cag atc cat | 1008 |
| Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His | |
| 325 330 335 | |
| | |
| gag acc atg aac att cgg cga ggg att atc aca gat tgg ttt ttc gga | 1056 |
| Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly | |
| 340 345 350 | |
| | |
| ggc ttg aac tac cag atc gag cac cat ttg tgg ccg acc ctc cct cgc | 1104 |
| Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg | |
| 355 360 365 | |
| | |
| cac aac ctg aca gcg gtt agc tac cag gtg gaa cag ctg tgc cag aag | 1152 |
| His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys | |
| 370 375 380 | |
| | |
| cac aac ctg ccg tat cgg aac ccg ctg ccc cat gaa ggg ttg gtc atc | 1200 |
| His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile | |
| 385 390 395 400 | |
| | |
| ctg ctg cgc tat ctg gcg gtg ttc gcc cgg atg gcg gag aag caa ccc | 1248 |
| Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro | |
| 405 410 415 | |
| | |
| gcg ggg aag gct cta taa | 1266 |
| Ala Gly Lys Ala Leu | |

<210> 2
 <211> 421
 <212> PRT
 <213> *Euglena gracilis*

<400> 2

Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr
 1 5 10 15

Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile
 20 25 30

Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met
 35 40 45

His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn
 50 55 60

Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu
 65 70 75 80

Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp
 85 90 95

Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu
 100 105 110

Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile
 115 120 125

Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser
 130 135 140

His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn
 145 150 155 160

Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr
 165 170 175

Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln
 180 185 190

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Gly | His | Asp | Pro | Asp | Ile | Asp | Asn | Leu | Pro | Leu | Leu | Ala | Trp | Ser | Glu | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Asp | Asp | Val | Thr | Arg | Ala | Ser | Pro | Ile | Ser | Arg | Lys | Leu | Ile | Gln | Phe | |
| | | 210 | | | | 215 | | | | | 220 | | | | | |
| Gln | Gln | Tyr | Tyr | Phe | Leu | Val | Ile | Cys | Ile | Leu | Leu | Arg | Phe | Ile | Trp | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Cys | Phe | Gln | Ser | Val | Leu | Thr | Val | Arg | Ser | Leu | Lys | Asp | Arg | Asp | Asn | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| Gln | Phe | Tyr | Arg | Ser | Gln | Tyr | Lys | Lys | Glu | Ala | Ile | Gly | Leu | Ala | Leu | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| His | Trp | Thr | Leu | Lys | Ala | Leu | Phe | His | Leu | Phe | Phe | Met | Pro | Ser | Ile | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| Leu | Thr | Ser | Leu | Leu | Val | Phe | Phe | Val | Ser | Glu | Leu | Val | Gly | Gly | Phe | |
| | | 290 | | | | 295 | | | | | 300 | | | | | |
| Gly | Ile | Ala | Ile | Val | Val | Phe | Met | Asn | His | Tyr | Pro | Leu | Glu | Lys | Ile | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| Gly | Asp | Ser | Val | Trp | Asp | Gly | His | Gly | Phe | Ser | Val | Gly | Gln | Ile | His | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| Glu | Thr | Met | Asn | Ile | Arg | Arg | Gly | Ile | Ile | Thr | Asp | Trp | Phe | Phe | Gly | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |
| Gly | Leu | Asn | Tyr | Gln | Ile | Glu | His | His | Leu | Trp | Pro | Thr | Leu | Pro | Arg | |
| | | 355 | | | | | 360 | | | | | 365 | | | | |
| His | Asn | Leu | Thr | Ala | Val | Ser | Tyr | Gln | Val | Glu | Gln | Leu | Cys | Gln | Lys | |
| | | 370 | | | | 375 | | | | | 380 | | | | | |
| His | Asn | Leu | Pro | Tyr | Arg | Asn | Pro | Leu | Pro | His | Glu | Gly | Leu | Val | Ile | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | |
| Leu | Leu | Arg | Tyr | Leu | Ala | Val | Phe | Ala | Arg | Met | Ala | Glu | Lys | Gln | Pro | |
| | | | | 405 | | | | | 410 | | | | | 415 | | |

Ala Gly Lys Ala Leu
420

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<223> delta9-elongase

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Met Ala Leu Ala Asn Asp Ala Gly Glu Arg Ile Trp Ala Ala Val Thr
1 5 10 15

gac ccg gaa atc ctc att ggc acc ttc tcg tac ttg cta ctc aaa ccg 96
Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro
20 25 30

ctg ctc cgc aat tcc ggg ctg gtg gat gag aag aag ggc gca tac agg 144
Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg
35 40 45

acg tcc atg atc tgg tac aac gtt ctg ctg gcg ctc ttc tct gcg ctg 192
Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu
50 55 60

agc ttc tac gtg acg gcg acc gcc ctc ggc tgg gac tat ggt acg ggc 240
Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly
65 70 75 80

gcg tgg ctg cgc agg caa acc ggc gac aca ccg cag ccg ctc ttc cag 288
Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln
85 90 95

tgc ccg tcc ccg gtt tgg gac tcg aag ctc ttc aca tgg acc gcc aag 336
Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys
100 105 110

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Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu
115 120 125

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Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp
130 135 140

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Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met
145 150 155 160

ttt ttc aac tcg ttc att cac acc atc atg tac acc tac tac ggc ctc 528
Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu

| 165 | 170 | 175 | |
|---|-----|-----|-----|
| acc gcc gcc ggg tat aag ttc aag gcc aag ccg ctc atc acc gcg atg | | | 576 |
| Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met | | | |
| 180 | 185 | 190 | |
| cag atc tgc cag ttc gtg ggc ggc ttc ctg ttg gtc tgg gac tac atc | | | 624 |
| Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile | | | |
| 195 | 200 | 205 | |
| aac gtc ccc tgc ttc aac tcg gac aaa ggg aag ttg ttc agc tgg gct | | | 672 |
| Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala | | | |
| 210 | 215 | 220 | |
| ttc aac tat gca tac gtc ggc tcg gtc ttc ttg ctc ttc tgc cac ttt | | | 720 |
| Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe | | | |
| 225 | 230 | 235 | 240 |
| ttc tac cag gac aac ttg gca acg aag aaa tcg gcc aag gcg ggc aag | | | 768 |
| Phe Tyr Gln Asp Asn Leu Ala Thr Lys Lys Ser Ala Lys Ala Gly Lys | | | |
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| Met | Ala | Leu | Ala | Asn | Asp | Ala | Gly | Glu | Arg | Ile | Trp | Ala | Ala | Val | Thr |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Asp | Pro | Glu | Ile | Leu | Ile | Gly | Thr | Phe | Ser | Tyr | Leu | Leu | Leu | Lys | Pro |
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| Leu | Leu | Arg | Asn | Ser | Gly | Leu | Val | Asp | Glu | Lys | Lys | Gly | Ala | Tyr | Arg |
| | | 35 | | | | | 40 | | | | | | 45 | | |
| Thr | Ser | Met | Ile | Trp | Tyr | Asn | Val | Leu | Leu | Ala | Leu | Phe | Ser | Ala | Leu |
| | | 50 | | | | | 55 | | | | | 60 | | | |
| Ser | Phe | Tyr | Val | Thr | Ala | Thr | Ala | Leu | Gly | Trp | Asp | Tyr | Gly | Thr | Gly |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Ala | Trp | Leu | Arg | Arg | Gln | Thr | Gly | Asp | Thr | Pro | Gln | Pro | Leu | Phe | Gln |
| | | | | | 85 | | | | | 90 | | | | | 95 |

Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys
100 105 110

Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu
115 120 125

Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp
130 135 140

Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met
145 150 155 160

Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu
165 170 175

Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met
180 185 190

Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile
195 200 205

Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala
210 215 220

Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe
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Gln Leu

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Ala Lys His Asn Ala Ala Thr Ile Ser Thr Gln Glu Arg Leu Cys Ser
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ctg tct tcg ctc aaa ggc gaa gaa gtc tgc atc gac gga atc atc tat      144
Leu Ser Ser Leu Lys Gly Glu Glu Val Cys Ile Asp Gly Ile Ile Tyr
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gac ctc caa tca ttc gat cat ccc ggg ggt gaa acg atc aaa atg ttt      192
Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe
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ggt ggc aac gat gtc act gta cag tac aag atg att cac ccg tac cat      240
Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His
65          70          75          80

acc gag aag cat ttg gaa aag atg aag cgt gtc ggc aag gt

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